

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/586,229
Source: IFWP
Date Processed by STIC: 7/26/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 07/26/2006

PATENT APPLICATION: US/10/586,229

TIME: 14:17:48

Input Set : A:\50274.021003.SEQLIST.TXT

Output Set: N:\CRF4\07262006\J586229.raw

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4 <110> APPLICANT: VOLLMERS, Heinz Peter
5     MUELLER-HERMELINK, Hans Konrad
6     HENSEL, Frank
8 <120> TITLE OF INVENTION: Neoplasm-Specific Polypeptides and Their
9     Uses
11 <130> FILE REFERENCE: 50274/021003
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/586,229
C--> 13 <141> CURRENT FILING DATE: 2006-07-19
13 <150> PRIOR APPLICATION NUMBER: PCT/US05/02480
14 <151> PRIOR FILING DATE: 2005-01-26
16 <150> PRIOR APPLICATION NUMBER: US 10/764,730
17 <151> PRIOR FILING DATE: 2004-01-26
19 <160> NUMBER OF SEQ ID NOS: 30
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 288
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)...(288)
32 <400> SEQUENCE: 1
33 tcc tgc aag gct tct ggc tac acc ttc act gac tac tat ata aac tgg      48
34 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp
35 1      5      10      15
37 gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag att tat      96
38 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
39      20      25      30
41 cct gga agt ggt aat act tac tac aat gag aag ttc aag ggc aag gcc      144
42 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
43      35      40      45
45 aca ctg act gca gac aaa tcc tcc agc aca gcc tac atg cag ctc agc      192
46 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
47      50      55      60
49 agc ctg aca tct gag gac tct gca gtc tat ttc tgt gca aga tcg gga      240
50 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
51 65      70      75      80
53 tta cga ccc tat gct atg gac tac tgg ggt caa gga acc tca gtc acc      288
54 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
55      85      90      95
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 96
61 <212> TYPE: PRT

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62 <213> ORGANISM: Mus musculus

64 <400> SEQUENCE: 2

65 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp

66 1 5 10 15

67 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr

68 20 25 30

69 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala

70 35 40 45

71 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser

72 50 55 60

73 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly

74 65 70 75 80

75 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr

76 85 90 95

79 <210> SEQ ID NO: 3

80 <211> LENGTH: 315

81 <212> TYPE: DNA

82 <213> ORGANISM: Mus musculus

84 <220> FEATURE:

85 <221> NAME/KEY: CDS

86 <222> LOCATION: (1)...(315)

88 <400> SEQUENCE: 3

89 cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 48

90 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys

91 1 5 10 15

93 aga tct agt cag agc att gta cat agt aat gga aac acc tat tta gaa 96

94 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu

95 20 25 30

97 tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg atc tac aaa 144

98 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys

99 35 40 45

101 gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 192

102 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly

103 50 55 60

105 tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat 240

106 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp

107 65 70 75 80

109 ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt ccg tac acg ttc 288

110 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe

111 85 90 95

113 gga ggg ggg acc aag ctg gaa ata aaa 315

114 Gly Gly Gly Thr Lys Leu Glu Ile Lys

115 100 105

118 <210> SEQ ID NO: 4

119 <211> LENGTH: 105

120 <212> TYPE: PRT

121 <213> ORGANISM: Mus musculus

123 <400> SEQUENCE: 4

124 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys

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125 1          5          10          15
126 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
127          20          25          30
128 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
129          35          40          45
130 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
131          50          55          60
132 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
133 65          70          75          80
134 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
135          85          90          95
136 Gly Gly Gly Thr Lys Leu Glu Ile Lys
137          100          105
140 <210> SEQ ID NO: 5
141 <211> LENGTH: 3114
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo sapiens
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)...(3114)
149 <400> SEQUENCE: 5
150 gat gtg agg gag cct gaa aat gaa att tct tca gac tgc aat cat ttg 48
151 Asp Val Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu
152 1          5          10          15
154 ttg tgg aat tat aag ctg aac cta act aca gat ccc aaa ttt gaa tct 96
155 Leu Trp Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser
156          20          25          30
158 gtg gcc aga gag gtt tgc aaa tct act ata aca gag att gaa gaa tgt 144
159 Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Glu Glu Cys
160          35          40          45
162 gct gat gaa ccg gtt gga aaa ggt tac atg gtt tcc tgc ttg gtg gat 192
163 Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp
164          50          55          60
166 cac cga ggc aac atc act gag tat cag tgt cac cag tac att acc aag 240
167 His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys
168 65          70          75          80
170 atg acg gcc atc att ttt agt gat tac cgt tta atc tgt ggc ttc atg 288
171 Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met
172          85          90          95
174 gat gac tgc aaa aat gac atc aac att ctg aaa tgt ggc agt att cgg 336
175 Asp Asp Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg
176          100          105          110
178 ctt gga gaa aag gat gca cat tca caa ggt gag gtg gta tca tgc ttg 384
179 Leu Gly Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu
180          115          120          125
182 gag aaa ggc ctg gtg aaa gaa gca gaa gaa aga gaa ccc aag att caa 432
183 Glu Lys Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln
184          130          135          140
186 gtt tct gaa ctc tgc aag aaa gcc att ctc cgg gtg gct gag ctg tca 480

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187 Val Ser Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser
188 145          150          155          160
190 tcg gat gac ttt cac tta gac cgg cat tta tat ttt gct tgc cga gat 528
191 Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp
192          165          170          175
194 gat cgg gag cgt ttt tgt gaa aat aca caa gct ggt gag ggc aga gtg 576
195 Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val
196          180          185          190
198 tat aag tgc ctc ttt aac cat aaa ttt gaa gaa tcc atg agt gaa aag 624
199 Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys
200          195          200          205
202 tgt cga gaa gca ctt aca acc cgc caa aag ctg att gcc cag gat tat 672
203 Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr
204          210          215          220
206 aaa gtc agt tat tca ttg gcc aaa tcc tgt aaa agt gac ttg aag aaa 720
207 Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys
208 225          230          235          240
210 tac cgg tgc aat gtg gaa aac ctt ccg cga tgc cgt gaa gcc agg ctc 768
211 Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu
212          245          250          255
214 tcc tac ttg tta atg tgc ctg gag tca gct gta cac aga ggg cga caa 816
215 Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln
216          260          265          270
218 gtc agc agt gag tgc cag ggg gag atg ctg gat tac cga cgc atg ttg 864
219 Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu
220          275          280          285
222 atg gaa gac ttt tct ctg agc cct gag atc atc cta agc tgt cgg ggg 912
223 Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly
224          290          295          300
226 gag att gaa cac cat tgt tcc gga tta cat cga aaa ggg cgg acc cta 960
227 Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu
228 305          310          315          320
230 cac tgt ctg atg aaa gta gtt cga ggg gag aag ggg aac ctt gga atg 1008
231 His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met
232          325          330          335
234 aac tgc cag cag gcg ctt caa aca ctg att cag gag act gac cct ggt 1056
235 Asn Cys Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly
236          340          345          350
238 gca gat tac cgc att gat cga gct ttg aat gaa gct tgt gaa tct gta 1104
239 Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val
240          355          360          365
242 atc cag aca gcc tgc aaa cat ata aga tct gga gac cca atg atc ttg 1152
243 Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu
244          370          375          380
246 tcg tgc ctg atg gaa cat tta tac aca gag aag atg gta gaa gac tgt 1200
247 Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys
248 385          390          395          400
250 gaa cac cgt ctc tta gag ctg cag tat ttc atc tcc cgg gat tgg aag 1248
251 Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys

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252		405		410		415	
254	ctg gac cct gtc ctg tac cgc aag tgc cag gga gac gct tct cgt ctt						1296
255	Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu						
256		420		425		430	
258	tgc cac acc cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga						1344
259	Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly						
260		435		440		445	
262	gct gtg ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag						1392
263	Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln						
264		450		455		460	
266	gga agg agg ctc tca cgg gag tgc cga gct gaa gtc caa agg atc cta						1440
267	Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu						
268	465		470		475		480
270	cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat aag						1488
271	His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys						
272		485		490		495	
274	tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag act gga						1536
275	Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly						
276		500		505		510	
278	cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta gtg gtg gag						1584
279	Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu						
280		515		520		525	
282	tgt aga gat ata gtt ggc aac ctc act gag tta gaa tca gag gat att						1632
283	Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile						
284		530		535		540	
286	caa ata gaa gcc ttg ctg atg aga gcc tgt gag ccc ata att cag aac						1680
287	Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn						
288	545		550		555		560
290	ttc tgc cac gat gtg gca gat aac cag ata gac tcc ggg gac ctg atg						1728
291	Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met						
292		565		570		575	
294	gag tgt ctg ata cag aac aaa cac cag aag gac atg aac gag aag tgt						1776
295	Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys						
296		580		585		590	
298	gcc atc gga gtt acc cac ttc cag ctg gtg cag atg aag gat ttt cgg						1824
299	Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg						
300		595		600		605	
302	ttt tct tac aag ttt aaa atg gcc tgc aag gag gac gtg ttg aag ctt						1872
303	Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu						
304		610		615		620	
306	tgc cca aac ata aaa aag aag gtg gac gtg gtg atc tgc ctg agc acg						1920
307	Cys Pro Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr						
308	625		630		635		640
310	acc gtg cgc aat gac act ctg cag gaa gcc aag gag cac agg gtg tcc						1968
311	Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser						
312		645		650		655	
314	ctg aag tgc cgc agg cag ctc cgt gtg gag gag ctg gag atg acg gag						2016
315	Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu						
316		660		665		670	

VERIFICATION SUMMARY

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Input Set : A:\50274.021003.SEQLIST.TXT

Output Set: N:\CRF4\07262006\J586229.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1059 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:1057

L:1099 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:1097